

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/839,136

DATE: 11/08/2001

TIME: 12:15:49

Input Set : A:\2356-7 Sequence Listing.txt

Output Set: N:\CRF3\11082001\I839136.raw

4 <110> APPLICANT: Naoyuki TANIGUCHI et al.
6 <120> TITLE OF INVENTION: ALPHA 1-6 FUCOSYLTRANSFERASE
9 <130> FILE REFERENCE: 2356-7
11 <140> CURRENT APPLICATION NUMBER: 09/839,136
12 <141> CURRENT FILING DATE: 2001-04-23
14 <150> PRIOR APPLICATION NUMBER: 09/442,629
15 <151> PRIOR FILING DATE: 1999-11-18
17 <150> PRIOR APPLICATION NUMBER: 08/913,805
18 <151> PRIOR FILING DATE: 1998-01-07
20 <150> PRIOR APPLICATION NUMBER: PCT/JP97/00171
21 <151> PRIOR FILING DATE: 1997-01-23
23 <160> NUMBER OF SEQ ID NOS: 15
25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1728
29 <212> TYPE: DNA
30 <213> ORGANISM: Pig
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (1)...(1728)
36 <400> SEQUENCE: 1

37	atg	cgg	cca	tgg	act	ggt	tgc	tgg	cgt	tgg	att	atg	ctc	att	ctt	ttt	48
38	Met	Arg	Pro	Trp	Thr	Gly	Ser	Trp	Arg	Trp	Ile	Met	Leu	Ile	Leu	Phe	
39	1				5					10					15		
41	gcc	tgg	ggg	acc	ttg	cta	ttt	tac	ata	ggt	ggt	cac	ttg	gta	cga	gat	96
42	Ala	Trp	Gly	Thr	Leu	Leu	Phe	Tyr	Ile	Gly	Gly	His	Leu	Val	Arg	Asp	
43				20					25					30			
45	aat	gac	cac	tct	gat	cac	tct	agc	cga	gaa	ctg	tcc	aag	att	ttg	gca	144
46	Asn	Asp	His	Ser	Asp	His	Ser	Ser	Arg	Glu	Leu	Ser	Lys	Ile	Leu	Ala	
47				35				40					45				
49	aag	ctg	gaa	cgc	tta	aaa	caa	caa	aat	gaa	gac	ttg	agg	aga	atg	gct	192
50	Lys	Leu	Glu	Arg	Leu	Lys	Gln	Gln	Asn	Glu	Asp	Leu	Arg	Arg	Met	Ala	
51		50					55				60						
53	gga	tct	ctc	cga	ata	cca	gaa	ggc	ccc	att	gat	cag	ggg	cca	gct	tca	240
54	Gly	Ser	Leu	Arg	Ile	Pro	Glu	Gly	Pro	Ile	Asp	Gln	Gly	Pro	Ala	Ser	
55	65				70					75					80		
57	gga	aga	gtt	cgt	gct	tta	gaa	gag	caa	ttt	atg	aag	gcc	aaa	gaa	cag	288
58	Gly	Arg	Val	Arg	Ala	Leu	Glu	Glu	Gln	Phe	Met	Lys	Ala	Lys	Glu	Gln	
59				85					90					95			
61	att	gaa	aat	tat	aag	aaa	caa	act	aaa	aat	ggt	cca	ggg	aag	gat	cat	336
62	Ile	Glu	Asn	Tyr	Lys	Lys	Gln	Thr	Lys	Asn	Gly	Pro	Gly	Lys	Asp	His	
63				100				105					110				
65	gaa	atc	cta	agg	agg	agg	att	gaa	aat	gga	gct	aaa	gag	ctc	tgg	ttt	384
66	Glu	Ile	Leu	Arg	Arg	Arg	Ile	Glu	Asn	Gly	Ala	Lys	Glu	Leu	Trp	Phe	
67				115				120					125				
69	ttt	cta	caa	agt	gag	ttg	aag	aaa	tta	aag	aat	tta	gaa	gga	aat	gaa	432
70	Phe	Leu	Gln	Ser	Glu	Leu	Lys	Lys	Leu	Lys	Asn	Leu	Glu	Gly	Asn	Glu	

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71	130	135	140	
73	ctc	caa	aga	cat gca gat gaa ttt cta tca gat ttg gga cat cat gaa 480
74	Leu	Gln	Arg His Ala Asp Glu Phe Leu Ser Asp Leu Gly His His Glu	
75	145	150	155	160
77	agg	tct	ata atg acg gat cta tac tac ctc agt caa aca gat ggg gca 528	
78	Arg	Ser	Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala	
79	165	170	175	
81	ggt	gat	tgg cgt gaa aag gag gcc aaa gat ctg aca gag ctg gtc cag 576	
82	Gly	Asp	Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln	
83	180	185	190	
85	cgg	aga	ata aca tat ctt cag aat ccc aag gac tgc agc aaa gcc aag 624	
86	Arg	Arg	Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Lys	
87	195	200	205	
89	aag	cta	gtg tgt aat atc aac aaa ggc tgt ggc tat ggc tgt cag ctc 672	
90	Lys	Leu	Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu	
91	210	215	220	
93	cat	cat	gta gtg tac tgc ttt atg att gca tat ggc acc cag cga aca 720	
94	His	His	Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr	
95	225	230	235	240
97	ctc	gcc	ttg gaa tct cac aat tgg cgc tac gct act ggg gga tgg gaa 768	
98	Leu	Ala	Leu Glu Ser His Asn Trp Arg Tyr Ala Thr Gly Gly Trp Glu	
99	245	250	255	
101	act	gtg	ttt aga cct gta agt gag acg tgc aca gac aga tct ggc agc 816	
102	Thr	Val	Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Ser	
103	260	265	270	
105	tcc	act	gga cat tgg tca ggt gaa gta aag gac aaa aat gtt cag gtg 864	
106	Ser	Thr	Gly His Trp Ser Gly Glu Val Lys Asp Lys Asn Val Gln Val	
107	275	280	285	
109	gtt	gag	ctc ccc att gta gac agt gtt cat cct cgt cct cca tat tta 912	
110	Val	Glu	Leu Pro Ile Val Asp Ser Val His Pro Arg Pro Pro Tyr Leu	
111	290	295	300	
113	ccc	ctg	gct gtc cca gaa gac ctt gca gat cga ctt gta cga gtc cat 960	
114	Pro	Leu	Ala Val Pro Glu Asp Leu Ala Asp Arg Leu Val Arg Val His	
115	305	310	315	320
117	ggt	gat	cct gca gtg tgg tgg gta tcc cag ttt gtc aag tac ttg att 1008	
118	Gly	Asp	Pro Ala Val Trp Trp Val Ser Gln Phe Val Lys Tyr Leu Ile	
119	325	330	335	
121	cgc	cca	caa ccc tgg ctg gaa aag gaa ata gaa gag gcc acc aag aag 1056	
122	Arg	Pro	Gln Pro Trp Leu Glu Lys Glu Ile Glu Glu Ala Thr Lys Lys	
123	340	345	350	
125	cta	ggc	ttc aaa cat cca gtt att gga gtc cat gtt aga cgc aca gac 1104	
126	Leu	Gly	Phe Lys His Pro Val Ile Gly Val His Val Arg Arg Thr Asp	
127	355	360	365	
129	aaa	gtg	gga gcg gaa gca gcc ttc cat ccc att gag gaa tac acg gtg 1152	
130	Lys	Val	Gly Ala Glu Ala Ala Phe His Pro Ile Glu Glu Tyr Thr Val	
131	370	375	380	
133	cac	gtt	gaa gaa gac ttt cag ctt ctt gct cgc aga atg caa gtg gat 1200	
134	His	Val	Glu Glu Asp Phe Gln Leu Leu Ala Arg Arg Met Gln Val Asp	
135	385	390	395	400

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```

137 aaa aaa agg gtg tat ttg gcc aca gat gac cct gct ttg tta aaa gag 1248
138 Lys Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Ala Leu Leu Lys Glu
139 405 410 415
141 gca aaa aca aag tac ccc agt tat gaa ttt att agt gat aac tct atc 1296
142 Ala Lys Thr Lys Tyr Pro Ser Tyr Glu Phe Ile Ser Asp Asn Ser Ile
143 420 425 430
145 tct tgg tca gct gga cta cat aat cga tat aca gaa aat tca ctt cgg 1344
146 Ser Trp Ser Ala Gly Leu His Asn Arg Tyr Thr Glu Asn Ser Leu Arg
147 435 440 445
149 ggt gtg atc ctg gat ata cac ttt ctc tcc cag gca gac ttc cta gtg 1392
150 Gly Val Ile Leu Asp Ile His Phe Leu Ser Gln Ala Asp Phe Leu Val
151 450 455 460
153 tgt act ttt tca tcg cag gtc tgt aga gtt gct tat gaa atc atg caa 1440
154 Cys Thr Phe Ser Ser Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln
155 465 470 475 480
157 gcg ctg cat cct gat gcc tct gag aac ttc cgt tct ttg gat gac atc 1488
158 Ala Leu His Pro Asp Ala Ser Ala Asn Phe Arg Ser Leu Asp Asp Ile
159 485 490 495
161 tac tat ttt gga ggc cca aat gcc cac aac caa att gcc att tat cct 1536
162 Tyr Tyr Phe Gly Gly Pro Asn Ala His Asn Gln Ile Ala Ile Tyr Pro
163 500 505 510
165 cac caa cct cga act gaa gga gaa atc ccc atg gaa cct gga gat att 1584
166 His Gln Pro Arg Thr Glu Gly Glu Ile Pro Met Glu Pro Gly Asp Ile
167 515 520 525
169 att ggt gtg gct gga aat cac tgg gat ggc tat cct aaa ggt gtt aac 1632
170 Ile Gly Val Ala Gly Asn His Trp Asp Gly Tyr Pro Lys Gly Val Asn
171 530 535 540
173 aga aaa ctg gga agg acg ggc cta tat ccc tcc tac aaa gtt cga gag 1680
174 Arg Lys Leu Gly Arg Thr Gly Leu Tyr Pro Ser Tyr Lys Val Arg Glu
175 545 550 555 560
177 aag ata gaa aca gtc aag tac ccc aca tat ccc gag gct gac aag taa 1728
178 Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Asp Lys *
179 565 570 575
183 <210> SEQ ID NO: 2
184 <211> LENGTH: 575
185 <212> TYPE: PRT
186 <213> ORGANISM: Pig
188 <400> SEQUENCE: 2
189 Met Arg Pro Trp Thr Gly Ser Trp Arg Trp Ile Met Leu Ile Leu Phe
190 1 5 10 15
191 Ala Trp Gly Thr Leu Leu Phe Tyr Ile Gly Gly His Leu Val Arg Asp
192 20 25 30
193 Asn Asp His Ser Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala
194 35 40 45
195 Lys Leu Glu Arg Leu Lys Gln Gln Asn Glu Asp Leu Arg Arg Met Ala
196 50 55 60
197 Gly Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Pro Ala Ser
198 65 70 75 80
199 Gly Arg Val Arg Ala Leu Glu Glu Gln Phe Met Lys Ala Lys Glu Gln

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200					85					90					95	
201	Ile	Glu	Asn	Tyr	Lys	Lys	Gln	Thr	Lys	Asn	Gly	Pro	Gly	Lys	Asp	His
202					100					105					110	
203	Glu	Ile	Leu	Arg	Arg	Arg	Ile	Glu	Asn	Gly	Ala	Lys	Glu	Leu	Trp	Phe
204					115					120				125		
205	Phe	Leu	Gln	Ser	Glu	Leu	Lys	Lys	Leu	Lys	Asn	Leu	Glu	Gly	Asn	Glu
206					130					135				140		
207	Leu	Gln	Arg	His	Ala	Asp	Glu	Phe	Leu	Ser	Asp	Leu	Gly	His	His	Glu
208					145					150				155		160
209	Arg	Ser	Ile	Met	Thr	Asp	Leu	Tyr	Tyr	Leu	Ser	Gln	Thr	Asp	Gly	Ala
210						165				170					175	
211	Gly	Asp	Trp	Arg	Glu	Lys	Glu	Ala	Lys	Asp	Leu	Thr	Glu	Leu	Val	Gln
212					180					185					190	
213	Arg	Arg	Ile	Thr	Tyr	Leu	Gln	Asn	Pro	Lys	Asp	Cys	Ser	Lys	Ala	Lys
214					195					200				205		
215	Lys	Leu	Val	Cys	Asn	Ile	Asn	Lys	Gly	Cys	Gly	Tyr	Gly	Cys	Gln	Leu
216					210					215				220		
217	His	His	Val	Val	Tyr	Cys	Phe	Met	Ile	Ala	Tyr	Gly	Thr	Gln	Arg	Thr
218					225					230				235		240
219	Leu	Ala	Leu	Glu	Ser	His	Asn	Trp	Arg	Tyr	Ala	Thr	Gly	Gly	Trp	Glu
220					245					250					255	
221	Thr	Val	Phe	Arg	Pro	Val	Ser	Glu	Thr	Cys	Thr	Asp	Arg	Ser	Gly	Ser
222					260					265					270	
223	Ser	Thr	Gly	His	Trp	Ser	Gly	Glu	Val	Lys	Asp	Lys	Asn	Val	Gln	Val
224					275					280				285		
225	Val	Glu	Leu	Pro	Ile	Val	Asp	Ser	Val	His	Pro	Arg	Pro	Pro	Tyr	Leu
226					290					295				300		
227	Pro	Leu	Ala	Val	Pro	Glu	Asp	Leu	Ala	Asp	Arg	Leu	Val	Arg	Val	His
228					305					310				315		320
229	Gly	Asp	Pro	Ala	Val	Trp	Trp	Val	Ser	Gln	Phe	Val	Lys	Tyr	Leu	Ile
230					325					330					335	
231	Arg	Pro	Gln	Pro	Trp	Leu	Glu	Lys	Glu	Ile	Glu	Glu	Ala	Thr	Lys	Lys
232					340					345					350	
233	Leu	Gly	Phe	Lys	His	Pro	Val	Ile	Gly	Val	His	Val	Arg	Arg	Thr	Asp
234					355					360				365		
235	Lys	Val	Gly	Ala	Glu	Ala	Ala	Phe	His	Pro	Ile	Glu	Glu	Tyr	Thr	Val
236					370					375				380		
237	His	Val	Glu	Glu	Asp	Phe	Gln	Leu	Leu	Ala	Arg	Arg	Met	Gln	Val	Asp
238					385					390				395		400
239	Lys	Lys	Arg	Val	Tyr	Leu	Ala	Thr	Asp	Asp	Pro	Ala	Leu	Leu	Lys	Glu
240					405					410					415	
241	Ala	Lys	Thr	Lys	Tyr	Pro	Ser	Tyr	Glu	Phe	Ile	Ser	Asp	Asn	Ser	Ile
242					420					425					430	
243	Ser	Trp	Ser	Ala	Gly	Leu	His	Asn	Arg	Tyr	Thr	Glu	Asn	Ser	Leu	Arg
244					435					440				445		
245	Gly	Val	Ile	Leu	Asp	Ile	His	Phe	Leu	Ser	Gln	Ala	Asp	Phe	Leu	Val
246					450					455				460		
247	Cys	Thr	Phe	Ser	Ser	Gln	Val	Cys	Arg	Val	Ala	Tyr	Glu	Ile	Met	Gln
248					465					470				475		480

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```

249 Ala Leu His Pro Asp Ala Ser Ala Asn Phe Arg Ser Leu Asp Asp Ile
250           485           490           495
251 Tyr Tyr Phe Gly Gly Pro Asn Ala His Asn Gln Ile Ala Ile Tyr Pro
252           500           505           510
253 His Gln Pro Arg Thr Glu Gly Glu Ile Pro Met Glu Pro Gly Asp Ile
254           515           520           525
255 Ile Gly Val Ala Gly Asn His Trp Asp Gly Tyr Pro Lys Gly Val Asn
256           530           535           540
257 Arg Lys Leu Gly Arg Thr Gly Leu Tyr Pro Ser Tyr Lys Val Arg Glu
258 545           550           555           560
259 Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Asp Lys
260           565           570           575
263 <210> SEQ ID NO: 3
264 <211> LENGTH: 26
265 <212> TYPE: PRT
266 <213> ORGANISM: Artificial Sequence
268 <220> FEATURE:
269 <223> OTHER INFORMATION: Primer
271 <400> SEQUENCE: 3
272 Lys Gln Thr Lys Asn Gly Pro Gly Lys Asp His Glu Ile Leu Arg Arg
273 1           5           10           15
274 Arg Ile Glu Asn Gly Ala Lys Glu Leu Gln
275           20           25
278 <210> SEQ ID NO: 4
279 <211> LENGTH: 10
280 <212> TYPE: PRT
281 <213> ORGANISM: Artificial Sequence
283 <220> FEATURE:
284 <223> OTHER INFORMATION: Primer
286 <400> SEQUENCE: 4
287 Lys Tyr Pro Thr Tyr Pro Glu Ala Asp Lys
288 1           5           10
291 <210> SEQ ID NO: 5
292 <211> LENGTH: 12
293 <212> TYPE: PRT
294 <213> ORGANISM: Artificial Sequence
296 <220> FEATURE:
297 <223> OTHER INFORMATION: Primer
299 <400> SEQUENCE: 5
300 Lys Tyr Leu Ile Arg Pro Gln Pro Trp Leu Glu Lys
301 1           5           10
304 <210> SEQ ID NO: 6
305 <211> LENGTH: 14
306 <212> TYPE: PRT
307 <213> ORGANISM: Artificial Sequence
309 <220> FEATURE:
310 <223> OTHER INFORMATION: Primer
312 <400> SEQUENCE: 6
313 Lys Arg Val Tyr Leu Ala Thr Asp Asp Pro Ala Leu Leu Lys

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/839,136

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L:334 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

L:353 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8